

logo

NTDB id 1284 ACE17W RS12370 WP 010946666.1	MRKIIAILII..ISASISLMAYSKDNSLISVKVLPLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDFISTDMQIPSDQ	78
NTDB id 1257 GC085 RS04855 WP 163621000.1	MRKIIAILIL..ISASISLAYSKDNSLISVKVLPLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDFISTDMQIPSDQ	78
NTDB id 186916 BBB50 RS01650 WP 000788426.1		0
NTDB id 1186 GTF74 RS01320 WP 000788426.1		0
NTDB id 1175 A1552VC RS12105 WP 000788426.1		0
NTDB id 1408 DSB67 RS13980 WP 010643500.1		0
NTDB id 1193 PAKAF RS26665 WP 003161249.1	MNSGLSRLGIALLAA.MFAPALLAADLEKLDVAALPGDRVELKQLQFDEPVA.APRGYTIEQPARTIALDLPGVQNKLG..T	76
NTDB id 1009 ACIAD RS15175 WP 004923730.1	MKQIIRQFSIGTVAYAIMQVASAQVAITNVVPMNIPGGTEIRVMFNGLPP.QPQAYQLEQPARLLIDFDKAGQKILA..K	77
NTDB id 1039 HON27 RS01460 WP 031993779.1	MNHVFRQFSMGAVAIAIMQAAASAQVSMTNIVPMQIAGQGTEIRVMFNGLPP.QPQAYQLENPSRLLIDFDKAQQGLK..Q	77
NTDB id 1052 ABD1 RS15850 WP 001017033.1	MNHVFRQFSMGAVAIAIMQAAASAQVSMTNIVPMQIAGQGTEIRVMFNGLPP.QPQAYQLENPSRLLIDFDKAQQGLK..Q	77
consensus	* * * * * * * * * * * * * * * * * *	

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NTDB id 1284 ACE17W RS12370 WP 010946666.1	STIITYTNEASVDVSDDDRRRLIYNLKNGLSYTTRVAGNLTWYVNSKQTSKHALCSSSPLPYVSVFSAE	145
NTDB id 1257 GC085 RS04855 WP 163621000.1	KTKTIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGSTAGSIYSLVLNGKSNDLFENSKE.....VFITNQV	145
NTDB id 186916 BBB50 RS01650 WP 000788426.1	KTKTIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGSTAGSVYSLVLNGKSNDLFENSKE.....VFITNQV	32
NTDB id 1186 GTF74 RS01320 WP 000788426.1	MKNGLKT..YVAQTLWTLWVG....LALCASS.....MVFSA.E	32
NTDB id 1175 A1552VC RS12105 WP 000788426.1	MKNGLKT..YVAQTLWTLWVG....LALCASS.....MVFSA.E	32
NTDB id 1408 DSB67 RS13980 WP 010643500.1	MKNGLKT..YVAQTLWTLWVG....LALCASS.....MVFSA.E	32
NTDB id 1193 PAKAF RS26665 WP 003161249.1	MKMRHGLTLTPRKLTGLFSLWFS....LLLAP.....FVAA.E	33
NTDB id 1009 ACIAD RS15175 WP 004923730.1	KNRELISVGNTRSVTVVEAKDRTRLIINLTTLSSTTRVEGNLNFVVGNSPAGASVASTAPVKASPAPASYAQPIKPKPY	156
NTDB id 1039 HON27 RS01460 WP 031993779.1	SLIPVTTNEASSIDVSSDDKRARVVVNLKDAAGFTTRVEGNVFILKINNIQSTAT.....PVAT..SA.....	138
NTDB id 1052 ABD1 RS15850 WP 001017033.1	SKISVATNEASSVDVTSDDQRSRLTVNLKDTGAFTTRVEGNTFILKINSAQTSNK.....PLPV..VS.....	138
consensus	* * * * * * * * * * * * * * * * * *	

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NTDB id 1284 ACE17W RS12370 WP 010946666.1	VNAKHEIKRIDFRGIEKQGGRLVIDVSDTGIPIDVTQVGKEIVVNFLNTKIPLNLMKRYDVSDFHSPVQIITMQQEGKKV	225
NTDB id 1257 GC085 RS04855 WP 163621000.1	VNAKHEIKRIDFRGIEKQGGRLVIDVSDTGIPIDVTQVGKEIVVNFLNTKIPLNLMKRYDVSDFHSPVQIITMQQEGKKV	225
NTDB id 186916 BBB50 RS01650 WP 000788426.1	SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPST	112
NTDB id 1186 GTF74 RS01320 WP 000788426.1	SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPST	112
NTDB id 1175 A1552VC RS12105 WP 000788426.1	SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPST	112
NTDB id 1408 DSB67 RS13980 WP 010643500.1	EVQSNLSKSIDFRTNKKDKDAVIVVELVSPAAIVDKIRVQEGLSIDLNTSVKDDQLYLLDVKDFSTVVESVEVFRDTSTT	113
NTDB id 1193 PAKAF RS26665 WP 003161249.1	VPAGRAIRNIDFQRGEKGENVVIDLSDPTLSPDIQEQQGKIRLDFAKTQLPDALRVRLDVKDFATPVQFVNASAQSDRT	236
NTDB id 1009 ACIAD RS15175 WP 004923730.1	PAPQQGIGNIGFQRGAQGEGLVVIDLQGTNTPVDVQQQGSKVVIRFPGIKIPHTLARRLNTTDFATPVASIDSYNDGSNG	218
NTDB id 1039 HON27 RS01460 WP 031993779.1	.AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQQGSKVVIRTIGTKIPHTLARRLNVNDFATPVSSIDAYNDKGVG	217
NTDB id 1052 ABD1 RS15850 WP 001017033.1	.AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQQGSKVVIRTIGTKIPHTLARRLNVNDFATPVSSIDAYNDKGVG	217
consensus	* * * * * * * * * * * * * * * * * *	

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NTDB id 1052 ABD1 RS15850 WP 001017033.1
consensus

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Position	Sequence	Score
1	RMTILSKG	305
2	RMTILSKG	305
3	QLVVTVD	191
4	QLVVTVD	191
5	QLVVTVD	191
6	RLVAYIDG	192
7	SITIEPSG	316
8	VISIQSTG	297
9	VITIQQSS	296
10	VITIQQSS	296

The sequence logo shows the conservation of residues across the alignment. The mutation site (position 100) is highlighted in red. The sequence is color-coded by amino acid type: basic (blue), acidic (red), polar (green), and non-polar (yellow).

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consensus

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[illegible]

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consensus

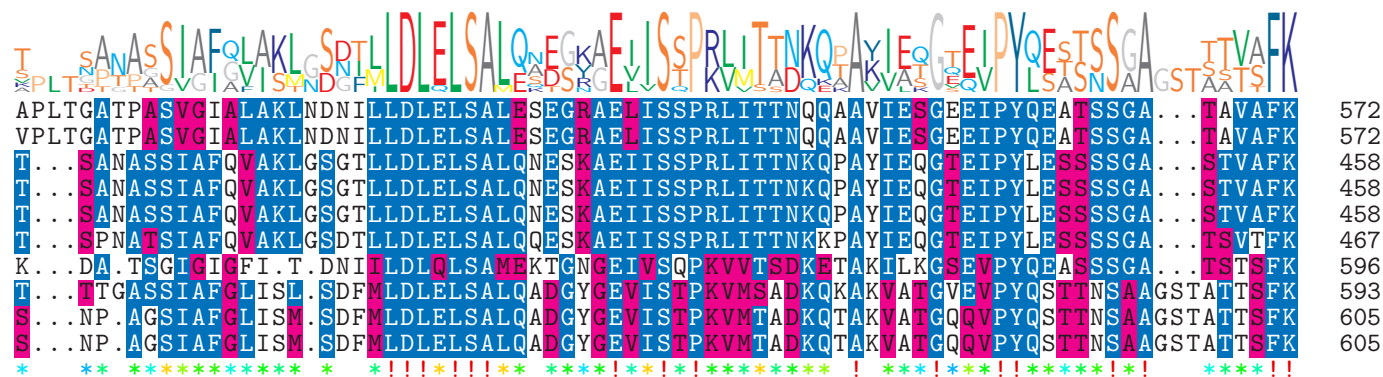
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[illegible]

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NTDB id 1284 ACE17W RS12370 WP 010946666.1
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consensus

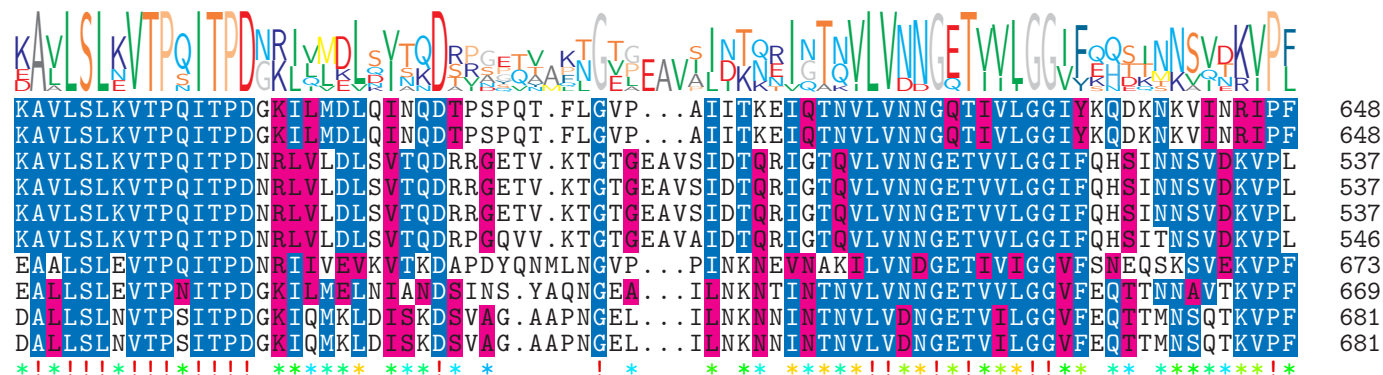
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NTDB id 1052 ABD1 RS15850 WP 001017033.1
consensus

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logo



X non conserved
X similar
X ≥ 50% conserved